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53

#### Raw Sequence Listing

SEQUENCE LISTING

06/25/91 10:32:10

#### Patent Application US/07/715,272

2 3 (1) GENERAL INFORMATION: (i) APPLICANT: Carter, Paul J. 5 6 Presta, Leonard G. 7 8 (ii) TITLE OF INVENTION: Immunoglobulin Variants 9 10 (iii) NUMBER OF SEQUENCES: 10 11 12 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Genentech, Inc. 13 14 (B) STREET: 460 Point San Bruno Blvd 15 (C) CITY: South San Francisco 16 (D) STATE: California 17 (E) COUNTRY: USA 18 (F) ZIP: 94080 19 20 (v) COMPUTER READABLE FORM: 21 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk 22 (B) COMPUTER: IBM PC compatible 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 24 (D) SOFTWARE: patin (Genentech) 25 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: 28 (B) FILING DATE: 14-June-1991 29 (C) CLASSIFICATION: 30 31 (vii) PRIOR APPLICATION DATA: 32 (A) APPLICATION NUMBER: 33 (B) FILING DATE: 34 (viii) ATTORNEY/AGENT INFORMATION: 35 36 (A) NAME: Adler, Carolyn R. 37 (B) REGISTRATION NUMBER: 32,324 38 (C) REFERENCE/DOCKET NUMBER: 709 39 40 (ix) TELECOMMUNICATION INFORMATION: 41 (A) TELEPHONE: 415/266-2614 42 (B) TELEFAX: 415/952-9881 43 (C) TELEX: 910/371-7168 44 45 (2) INFORMATION FOR SEQ ID NO:1: 46 47 (i) SEQUENCE CHARACTERISTICS: 48 (A) LENGTH: 109 amino acids 49 (B) TYPE: amino acid 50 (D) TOPOLOGY: linear 51 52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

54 55 56	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
57 58 59	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Ser	Gln	Asp	Val	Asn 30
60 61 62	Thr	Ala	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
63 64 65	Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Phe	Leu	Glu 55	Ser	Gly	Val	Pro	Ser 60
66 67 68	Arg	Phe	Ser	Gly	Ser 65	Arg	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
69 70 71			Leu		80					85		_	_		90
72 73 74			Thr		Pro 95	Pro	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
75 76 77		-	Arg	109											
78 79	(2)	INFO	RMAT	ION 1	FOR S	SEQ 1	ID NO	0:2:							
80	( :	i) Si	EQUE	NCE (	CHAR	ACTE	RIST	rcs.							
81		-	A) LI	engti	H: 12	20 ar	nino		ls						
82		(1	A) LI B) TY	ENGTI PE:	H: 12 amin	20 ar	nino cid		ls						
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82 83 84 85	( <b>x</b> :	(1	A) LI B) TY	ENGTI PE: OPOLO	H: 12 amir DGY:	20 ar no ac line	mino cid ear	acio		<b>10:2</b> :	<b>:</b>				
82 83 84 85 86		(1 (1 i) SI	A) LI B) TI D) TO	ENGTI (PE: OPOLO	H: 12 amin DGY: DESCE	20 ar no ac line	mino cid ear	acid	ID 1						
82 83 84 85 86 87 88	Glu 1	() () i) Si Val	A) LI B) TY D) TO EQUEN	ENGTI (PE: DPOLO NCE I	H: 12 amin DGY: DESCI Val	20 am no ac line RIPTI	nino cid ear ION:	SEQ Gly	ID 1	Gly 10	Leu				15
82 83 84 85 86 87	Glu 1	() () i) Si Val	A) LI B) TI D) TO	ENGTI (PE: DPOLO NCE I	H: 12 amin DGY: DESCI Val	20 am no ac line RIPTI	nino cid ear ION:	SEQ Gly	ID 1	Gly 10	Leu				15
82 83 84 85 86 87 88 89 90	Glu 1 Gly	(1 (1 i) SI Val Ser	A) LI B) TY D) TO EQUEN	ENGTH YPE: DPOLO NCE I Leu	H: 12 amin DGY: DESCI Val 5 Leu 20	20 ar no ac line RIPT: Glu Ser	nino cid ear ION: Ser	SEQ Gly	ID N Gly Ala	Gly 10 Ser 25	Leu Gly	Phe	Asn	Ile	15 Lys 30
82 83 84 85 86 87 88 89 90 91 92 93	Glu 1 Gly Asp	(I (I i) SI Val Ser	A) LI B) TY D) TO EQUEN Gln Leu	ENGTH YPE: DPOLO NCE I Leu Arg	H: 12 amin DGY: DESCI Val 5 Leu 20 His 35	20 am no ac line RIPT Glu Ser	nino cid car ION: Ser Cys	seQ Gly Ala	ID N Gly Ala Gln	Gly 10 Ser 25 Ala 40	Leu Gly Pro	Phe Gly	Asn Lys	Ile Gly	15 Lys 30 Leu 45
82 83 84 85 86 87 88 89 90 91 92 93 94 95	Glu 1 Gly Asp	(1) i) Si Val Ser Thr	A) LI B) TY C) TO EQUE  Gln  Leu  Tyr	ENGTI YPE: DPOLO NCE I Leu Arg Ile Ala	H: 12 amin DGY: DESCR Val 5 Leu 20 His 35 Arg 50	20 ar no ac line RIPTI Glu Ser Trp	mino cid car ION: Ser Cys Val	SEQ Gly Ala Arg	ID N Gly Ala Gln Thr	Gly 10 Ser 25 Ala 40 Asn 55	Leu Gly Pro Gly	Phe Gly Tyr	Asn Lys Thr	Ile Gly Arg	15 Lys 30 Leu 45 Tyr 60
82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98	Glu 1 Gly Asp Glu Ala	(1) (1) (1) (2) (3) (4) (4) (5) (7) (7) (7) (7) (7) (8) (8) (9) (9) (9) (9) (9) (9) (9) (9) (9) (9	A) LI B) TY COLUMN COLU	ENGTI YPE: DPOLO NCE I Leu Arg Ile Ala Val	H: 12 amin DGY: DESCH Val 5 Leu 20 His 35 Arg 50 Lys 65	20 am no ac line RIPT Glu Ser Trp Ile Gly	mino cid car CON: Ser Cys Val Tyr Arg	SEQ Gly Ala Arg Pro	ID N Gly Ala Gln Thr	Gly 10 Ser 25 Ala 40 Asn 55 Ile 70	Leu Gly Pro Gly Ser	Phe Gly Tyr	Asn Lys Thr	Ile Gly Arg	15 Lys 30 Leu 45 Tyr 60 Ser 75

Page: 3

### Raw Sequence Listing

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107															
108	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
109					110					115					120
110															
111	40	***													
112 113	(2)	INFO	RMAT:	ION I	FOR :	SEQ :	ID NO	0:3:							
114		i) S	EQUE	MOP 4	מ אשר	v Cure	D T CM	ree.							
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116		-	B) T					acr	45						
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119	(x:	i) S	EQUE	NCE 1	DESCI	RIPT	ION:	SEQ	ID I	NO:3	:				
120								_							
121	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
122	1				5					10					15
123															
124	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Val	Ser
125					20					25					30
126	_	_	_				_	_							
127	Ser	Tyr	Leu	Ala	_	Tyr	Gln	Gln	Lys		Gly	Lys	Ala	Pro	_
128					35					40					45
129 130	T 0	T 0	T1-	<b>M</b>	71-	<b>81</b> -	<b>G</b>		<b>.</b>	<b>a</b> 1				_	_
131	Leu	Leu	Ile	TYP	50	AIA	ser	ser	Leu		ser	GTĀ	val	Pro	
132					50					55					60
133	Ara	Phe	Ser	Glv	Ser	G1 <sub>w</sub>	Sar	Glw	Th =	Aen	Dho	mh =	Tou	mh	Tlo
134	••• 9		001	011	65	OII	361	GIY	1111	70	rne	1111	Leu	Int	75
135					•					, ,					,,
136	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tvr	Tvr	Cvs	Gln	Gln
137					80					85	-1-	-1-	-1-		90
138															
139	Tyr	Asn	Ser	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu
140					95				, -	100	-		-		105
141						*									
142	Ile	Lys	Arg	Thr											
143				109											
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145	(2)	INFO	RMAT:	CON I	FOR S	SEQ 1	D NO	):4:							
146	4	, , ,													
147 148	(:		EQUE												
149			A) LI B) Ti					acı	15						
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156					-										
157	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Glv	Phe	Thr	Phe	Ser
158	-			_	20		-			25	- 4				30
159															

160	Asp '	Tyr	Ala	Met		Trp	Val	Arg	Gln		Pro	Gly	Lys	Gly	
161					35					40					45
162		_								_	_				
163	Glu !	Trp	Val	Ala		Ile	Ser	Glu	Asn		Gly	Tyr	Thr	Arg	Tyr
164					50					55					60
165															
166	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser
167					65					70					75
168															
169	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
170					80					85					90
171															
172	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr
173					95					100					105
174															
175	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
176			_		110	_		_		115					120
177									•						
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179	(2) I	NFOE	MAT	ON I	FOR S	SEO :	ID NO	0:5:							
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188	B === '	<b>*</b> 1 -	**- 1	<b>1</b> /	mb	<b>01</b>		77 / -	<b>-</b>		30-1			_	
189	Asp :	116	vai	Met		GIN	ser	HIS	гÃ2		Met	ser	Thr	ser	
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190	<b>61</b>			•• - 1				_	_		_		_		
191	Gly i	Asp	Arg	val		IIe	Thr	Cys	Lys		Ser	Gln	Asp	Val	
192					20					25					30
193							_	_							
194	Thr I	Ala	Val	Ala		Tyr	Gln	Gln	Lys	Pro	Gly	His	Ser	Pro	Lys
195					35					40					45
196															
197	Leu l	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Arg	Tyr	Thr	Gly	Val	Pro	Asp
198					50					55					60
199															
200	Arg 1	Phe	Thr	Gly	Asn	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile
201					65					70					75
202															
203	Ser :	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tvr	Tvr	Cvs	Gln	Gln
204					80		•			85	-	•	_		90
205					-										
206	His !	[vr	Thr	Thr	Pro	Pro	Thr	Phe	Glv	Glv	Glv	Thr	Lvc	Len	Glu
207					95				1	100	1		-13	Lu	105
208															103
			B	71-											
209	י פון	.ve													
209 210	Ile I	Lys	Arg												
210	ile i	Lys	Arg	109											
	(2) II	_		109	POP 6	· P.O	. D. 37	<b></b> .							

213														
214	(i)	SEQUE												
215		(A) L	engti	H: 13	20 aı	mino	acio	ds						
216		(B) T	YPE:	ami	no a	cid								
217		(D) T	OPOL	OGY:	line	ear								
218														
219	(xi)	SEQUE	NCE I	DESC	RIPT	ION:	SEQ	ID I	NO:6	:				
220														
221	Glu V	al Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly
222	1			5					10					15
223														
224	Ala S	er Leu	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys
225				20					25					30
226														
227	Asp T	hr Tyr	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Lev
228				35					40					45
229	_													
230	Glu T	rp Ile	Gly	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr
231				50					55					60
232		_												
233	Asp P	co Lys	Phe		Asp	Lys	Ala	Thr		Thr	Ala	Asp	Thr	Ser
234				65					70					75
235				_		_	_							
236	Ser A	sn Thr	Ala		Leu	Gln	Val	Ser	Arg	Leu	Thr	Ser	Glu	_
237				80					85					90
238														
239	Thr A	la Val	Tyr		Cys	Ser	Arg	Trp	_	Gly	Asp	Gly	Phe	Tyr
240				95					100					105
241			_			_	_							
242	Ala Me	et Asp	Tyr		Gly	Gln	Gly	Ala		Val	Thr	Val	Ser	
243				110					115					120
244														
245	/0\ T\													
246	(2) INI	ORMAT.	CON I	FOR S	SEQ 1	ID NO	0:7:							
247														
248	(1)	SEQUE					ics:							
249		(A) LI												
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	(X1)	SEQUE	ACE I	DESC	KIPTI	LON:	SEQ	ID I	10:7	3				
255														
256		magazz	n n <i>m a c</i>				amaa							
257 258		TCCGAT	CATC	: AG(	JTGA(	CCA	GTCI	CCA	27					
259														
260	/2\ T***			70E -	· -									
261	(2) INF	UKMAT	LON F	OR S	SEQ 1	א ענו	ງ: 8:							
262	495													
263	(1)	SEQUE					CS:							
264 265		(A) Li												
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#### Raw Sequence Listing

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### Patent Application US/07/715,272

266 267	(C) STRANDEDNESS: single (D) TOPOLOGY: linear
268 269 270	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
271 272 273	GTTGATCTC CAGCTTGGTA COXXCDCCGA A 31 are not valid according
274 275	
276 277	(2) INFORMATION FOR SEQ ID NO:9:
278	(i) SEQUENCE CHARACTERISTICS:
279	(A) LENGTH: 22 bases
280	(B) TYPE: nucleic acid
281	(C) STRANDEDNESS: single
282	(D) TOPOLOGY: linear
283 284	(wi) SPOUPAGE DESCRIPTION, ORG. ID NO. C.
285	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
286	
287	AGGTXXAXCT GCAGXAGTCX GG 22
288	AGGIRANACI GCAGAAGICA/GG 22
289	
290	
291	(2) INFORMATION FOR SEQ ID NO:10:
292	(-,
293	(i) SEQUENCE CHARACTERISTICS:
294	(A) LENGTH: 34 bases
295	(B) TYPE: nucleic acid
296	(C) STRANDEDNESS: single
297	(D) TOPOLOGY: linear
298	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGAGGAGACG GTGACCGTGG TCCCTTGGCC CCAG 34

PAGE: 1

#### SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/715,272

DATE: 06/25/91 TIME: 10:32:20

LINE ERROR

#### ORIGINAL TEXT

Wrong Nucleic Acid Designator

269 Entered and Calc. Seq. Length difference (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGIXFAXCT GCAGXAGTCX GG 22

CONTROL DESCRIPTION: SEO ID NO:9:

284 Entered and Calc. Seq. Length differ (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/715,272

DATE: 06/25/91 TIME: 10:32:20

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PAGÉ: 1

LINE ORIGINAL TEXT

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/715,272

CORRECTED TEXT

DATE: 06/25/91 TIME: 10:32:20